



SEQUENCE LISTING

#5

<110> Millennium Pharmaceuticals, Inc.
Glucksmann, Maria
Tsai, Fong-Ying

<120> 27439, NOVEL HUMAN HYDROXYLASE AND USES
THEREFOR

<130> 38155-20036.00

<140> US 09/945,301

<141> 2001-08-31

<150> US 60/229,301

<151> 2000-09-01

<160> 16

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1976

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1614)

<221> misc_feature

<222> (1)...(1976)

<223> n = A,T,C or G

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Met Ala Leu Leu Ala Arg Ile Leu Arg Ala Gly Leu Arg Pro Ala Pro
1 5 10 15

gag cgg ggt ggg ctc ctg ggc ggc ggg gcc ccg cgg cgg cct caa ccc 96
Glu Arg Gly Gly Leu Leu Gly Gly Gly Ala Pro Arg Arg Pro Gln Pro
20 25 30

gcg ggc gca cgg ctc ccg gcg ggg gcg cgg gcc gag gac aaa ggc gcc 144
Ala Gly Ala Arg Leu Pro Ala Gly Ala Arg Ala Glu Asp Lys Gly Ala
35 40 45

ggg cgg ccg ggg tcg ccg ccg gga ggg ggc cga gcc gag ggt ccc cgg 192
Gly Arg Pro Gly Ser Pro Pro Gly Gly Gly Arg Ala Glu Gly Pro Arg
50 55 60

agc ctc gcc gcc atg ccg ggg ccg agg acc ctc gcc aac ctg gcg gag 240
Ser Leu Ala Ala Met Pro Gly Pro Arg Thr Leu Ala Asn Leu Ala Glu
65 70 75 80

ttc ttc tgc agg gac ggc ttc agc cgc atc cac gag atc cag cag aag 288

Phe	Phe	Cys	Arg	Asp	Gly	Phe	Ser	Arg	Ile	His	Glu	Ile	Gln	Gln	Lys		
				85					90					95			
cac	aca	cgg	gaa	tat	gga	aaa	atc	ttc	aag	tct	cac	ttt	ggg	cct	cag	336	
His	Thr	Arg	Glu	Tyr	Gly	Lys	Ile	Phe	Lys	Ser	His	Phe	Gly	Pro	Gln		
			100					105					110				
ttt	gta	gta	tct	att	gca	gac	cgc	gat	atg	gtg	gct	cag	gtg	ctc	cgg	384	
Phe	Val	Val	Ser	Ile	Ala	Asp	Arg	Asp	Met	Val	Ala	Gln	Val	Leu	Arg		
			115				120					125					
gcg	gag	ggc	gct	gcg	ccc	cag	aga	gcc	aac	atg	gag	tcc	tgg	cgg	gag	432	
Ala	Glu	Gly	Ala	Ala	Pro	Gln	Arg	Ala	Asn	Met	Glu	Ser	Trp	Arg	Glu		
	130					135					140						
tac	cga	gac	ttg	cgg	ggg	aga	gcc	acc	ggg	ctc	atc	tcg	gcg	gag	ggg	480	
Tyr	Arg	Asp	Leu	Arg	Gly	Arg	Ala	Thr	Gly	Leu	Ile	Ser	Ala	Glu	Gly		
145					150					155					160		
gaa	cag	tgg	ctc	aag	atg	aga	agc	gta	ttg	aga	caa	aga	att	ctg	aaa	528	
Glu	Gln	Trp	Leu	Lys	Met	Arg	Ser	Val	Leu	Arg	Gln	Arg	Ile	Leu	Lys		
				165					170					175			
ccg	aaa	gat	gtg	gcc	att	tat	tct	gga	gaa	gtc	gac	caa	gtt	att	gct	576	
Pro	Lys	Asp	Val	Ala	Ile	Tyr	Ser	Gly	Glu	Val	Asp	Gln	Val	Ile	Ala		
			180					185					190				
gac	tta	att	aaa	aga	atc	tac	ctc	ctc	agg	agc	cag	gca	gaa	gat	gga	624	
Asp	Leu	Ile	Lys	Arg	Ile	Tyr	Leu	Leu	Arg	Ser	Gln	Ala	Glu	Asp	Gly		
		195					200					205					
gaa	acc	gtg	acc	aat	gtc	aat	gat	ctt	ttc	ttc	aaa	tat	tca	atg	gaa	672	
Glu	Thr	Val	Thr	Asn	Val	Asn	Asp	Leu	Phe	Phe	Lys	Tyr	Ser	Met	Glu		
	210					215					220						
gga	gtg	gcc	acc	atc	ctt	tat	gag	agt	cgt	ttg	ggc	tgc	ctg	gaa	aac	720	
Gly	Val	Ala	Thr	Ile	Leu	Tyr	Glu	Ser	Arg	Leu	Gly	Cys	Leu	Glu	Asn		
225					230				235						240		
agc	atc	cca	cag	ctg	act	gtg	gaa	tac	atc	gag	gcc	ctg	gag	ctc	atg	768	
Ser	Ile	Pro	Gln	Leu	Thr	Val	Glu	Tyr	Ile	Glu	Ala	Leu	Glu	Leu	Met		
				245					250					255			
ttt	agc	atg	ttc	aag	acc	tcc	atg	tat	gca	ggc	gcc	atc	ccc	aga	tgg	816	
Phe	Ser	Met	Phe	Lys	Thr	Ser	Met	Tyr	Ala	Gly	Ala	Ile	Pro	Arg	Trp		
			260					265					270				
ctt	cgc	ccc	ttc	atc	cca	aag	ccc	tgg	cgg	gaa	ttc	tgc	agg	tcc	tgg	864	
Leu	Arg	Pro	Phe	Ile	Pro	Lys	Pro	Trp	Arg	Glu	Phe	Cys	Arg	Ser	Trp		
		275					280					285					
gat	gga	ctc	ttc	aaa	ttc	agc	caa	att	cat	gtt	gac	aac	aag	ttg	tgg	912	
Asp	Gly	Leu	Phe	Lys	Phe	Ser	Gln	Ile	His	Val	Asp	Asn	Lys	Leu	Trp		
	290					295					300						
gac	ata	cag	tac	caa	atg	gac	cga	ggc	cgg	agg	gtg	agc	ggg	gga	ctt	960	
Asp	Ile	Gln	Tyr	Gln	Met	Asp	Arg	Gly	Arg	Arg	Val	Ser	Gly	Gly	Leu		

305	310	315	320	
ctc aca tac ctc ttc ctt agc cag gct ctg acg ctg cag gag atc tac				1008
Leu Thr Tyr Leu Phe Leu Ser Gln Ala Leu Thr Leu Gln Glu Ile Tyr				
325		330	335	
gcc aac gtg act gag atg ctg ctg gcc ggc gtc gac acg acg tcc ttc				1056
Ala Asn Val Thr Glu Met Leu Leu Ala Gly Val Asp Thr Thr Ser Phe				
340		345	350	
acc ttg tct tgg acg gtg tac ctc ctg gca agg cac cca gaa gtg cag				1104
Thr Leu Ser Trp Thr Val Tyr Leu Leu Ala Arg His Pro Glu Val Gln				
355		360	365	
cag acg gtg tac cgg gag att gtg aag aat tta ggg gaa agg cat gtt				1152
Gln Thr Val Tyr Arg Glu Ile Val Lys Asn Leu Gly Glu Arg His Val				
370		375	380	
cca act gca gct gat gtc ccc aag gtc ccg ctg gtc aga gct ctc ctt				1200
Pro Thr Ala Ala Asp Val Pro Lys Val Pro Leu Val Arg Ala Leu Leu				
385		390	395	400
aag gaa acc ctg agg ctg ttt cca gtg ctg cca ggg aac ggc cgg gtc				1248
Lys Glu Thr Leu Arg Leu Phe Pro Val Leu Pro Gly Asn Gly Arg Val				
405		410	415	
acc cag gaa gac ctg gtt att ggc ggg tat ctg att ccg aaa ggc acc				1296
Thr Gln Glu Asp Leu Val Ile Gly Gly Tyr Leu Ile Pro Lys Gly Thr				
420		425	430	
cag ctg gcc ctt tgc cac tat gcc aca tcg cac cag gat gag aac ttc				1344
Gln Leu Ala Leu Cys His Tyr Ala Thr Ser His Gln Asp Glu Asn Phe				
435		440	445	
cct cgg gcc aag gag ttc cga cct gag cgc tgg ctg cgg aaa gga gac				1392
Pro Arg Ala Lys Glu Phe Arg Pro Glu Arg Trp Leu Arg Lys Gly Asp				
450		455	460	
tta gat aga gtt gac aat ttt gga tcc atc ccc ttt ggt cat ggg gtt				1440
Leu Asp Arg Val Asp Asn Phe Gly Ser Ile Pro Phe Gly His Gly Val				
465		470	475	480
cgc agc tgc ata ggg cgg aga att gca gaa ctg gag att cac ctc gtc				1488
Arg Ser Cys Ile Gly Arg Arg Ile Ala Glu Leu Glu Ile His Leu Val				
485		490	495	
gtg atc cag ttg ctt caa cat ttt gag atc aaa aca tct tct cag acc				1536
Val Ile Gln Leu Leu Gln His Phe Gly Ile Lys Thr Ser Ser Gln Thr				
500		505	510	
aat gct gtt cat gca aaa acc cac ggg ctc ctg acg cca ggg ggg ccc				1584
Asn Ala Val His Ala Lys Thr His Gly Leu Leu Thr Pro Gly Gly Pro				
515		520	525	
atc cac gtg cga ttt gtt aac aga aag taa gcctagattt taaacctggg				1634
Ile His Val Arg Phe Val Asn Arg Lys *				
530		535		

ctgatgtagc agaccagctc gccgacacac agtgggtatt tgtgttcgct gatcacccgtg 1694
gagaaggaaa gcgatgtcgc taaaggctgt cttgttatag actggcctcc caggctcctgg 1754
gacacttgta aatctttatg caaagtaatg taaaaagggt gctattttac tgggtgcatac 1814
cagaagtgtc cctttctttg ggggaaacag ctgttttaaaa accagtggca gtgaattttt 1874
atgcttcata cattngcta gactcaatat ttaatgactg gcagtatcct gtgcattttac 1934
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<210> 2
<211> 537
<212> PRT
<213> Homo sapiens

<400> 2
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1 5 10 15
Glu Arg Gly Gly Leu Leu Gly Gly Gly Ala Pro Arg Arg Pro Gln Pro
20 25 30
Ala Gly Ala Arg Leu Pro Ala Gly Ala Arg Ala Glu Asp Lys Gly Ala
35 40 45
Gly Arg Pro Gly Ser Pro Pro Gly Gly Gly Arg Ala Glu Gly Pro Arg
50 55 60
Ser Leu Ala Ala Met Pro Gly Pro Arg Thr Leu Ala Asn Leu Ala Glu
65 70 75 80
Phe Phe Cys Arg Asp Gly Phe Ser Arg Ile His Glu Ile Gln Gln Lys
85 90 95
His Thr Arg Glu Tyr Gly Lys Ile Phe Lys Ser His Phe Gly Pro Gln
100 105 110
Phe Val Val Ser Ile Ala Asp Arg Asp Met Val Ala Gln Val Leu Arg
115 120 125
Ala Glu Gly Ala Ala Pro Gln Arg Ala Asn Met Glu Ser Trp Arg Glu
130 135 140
Tyr Arg Asp Leu Arg Gly Arg Ala Thr Gly Leu Ile Ser Ala Glu Gly
145 150 155 160
Glu Gln Trp Leu Lys Met Arg Ser Val Leu Arg Gln Arg Ile Leu Lys
165 170 175
Pro Lys Asp Val Ala Ile Tyr Ser Gly Glu Val Asp Gln Val Ile Ala
180 185 190
Asp Leu Ile Lys Arg Ile Tyr Leu Leu Arg Ser Gln Ala Glu Asp Gly
195 200 205
Glu Thr Val Thr Asn Val Asn Asp Leu Phe Phe Lys Tyr Ser Met Glu
210 215 220
Gly Val Ala Thr Ile Leu Tyr Glu Ser Arg Leu Gly Cys Leu Glu Asn
225 230 235 240
Ser Ile Pro Gln Leu Thr Val Glu Tyr Ile Glu Ala Leu Glu Leu Met
245 250 255
Phe Ser Met Phe Lys Thr Ser Met Tyr Ala Gly Ala Ile Pro Arg Trp
260 265 270
Leu Arg Pro Phe Ile Pro Lys Pro Trp Arg Glu Phe Cys Arg Ser Trp
275 280 285
Asp Gly Leu Phe Lys Phe Ser Gln Ile His Val Asp Asn Lys Leu Trp
290 295 300
Asp Ile Gln Tyr Gln Met Asp Arg Gly Arg Arg Val Ser Gly Gly Leu
305 310 315 320
Leu Thr Tyr Leu Phe Leu Ser Gln Ala Leu Thr Leu Gln Glu Ile Tyr
325 330 335
Ala Asn Val Thr Glu Met Leu Leu Ala Gly Val Asp Thr Thr Ser Phe

cttcaacatt ttgagatcaa aacatcttct cagaccaatg ctgttcatgc aaaaacccac 1560
 gggctcctga cgccaggggg gcccatccac gtgcgatttg ttaacagaaa gtaa 1614

<210> 4
 <211> 496
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

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 Gly Arg Ala Pro Gly Pro Ile Pro His Ser Leu Thr Lys Leu Arg Lys
 20 25 30
 Ala Lys Arg Tyr Gly Lys Pro Val Phe Thr Leu Tyr Leu Gly Pro Arg
 35 40 45
 Pro Val Val Val Leu Thr Gly Pro Glu Ala Val Lys Glu Val Leu Ile
 50 55 60
 Asp Lys Gly Glu Glu Phe Ala Lys Gly Arg Gly Asp Phe Asn Pro Thr
 65 70 75 80
 Phe Pro Trp Leu Ser Lys Gly Tyr Arg Glu Gln Gly Leu Leu Phe Ser
 85 90 95
 Asp Asn Gly Pro Lys Trp Arg Lys Leu Arg Arg Phe Ser Leu Leu Thr
 100 105 110
 Leu Arg Phe His Phe Gly Met Gly Ala Tyr Ser Lys Arg Ser Gln Lys
 115 120 125
 Leu Glu Glu Pro Arg Ile Gln Glu Glu Ala Arg Asp Leu Val Glu Arg
 130 135 140
 Leu Arg Lys Glu Gln Ala Gly Ser Pro Ile Asp Ile Thr Glu Leu Leu
 145 150 155 160
 Ala Arg Leu Ala Pro Leu Asn Val Ile Cys Ser Leu Leu Phe Gly Val
 165 170 175
 Arg Phe Asp Tyr Leu Arg Pro Glu Asp Pro Glu Phe Leu Lys Leu Ile
 180 185 190
 Asp Lys Leu Leu Asn Glu Met Phe Asp Arg Val Ser Pro Trp His Gln
 195 200 205
 Leu Leu Asp Ile Phe Pro Phe Leu Leu Arg Tyr Leu Pro Gly Ser Leu
 210 215 220
 Phe Arg Lys Ala Phe Lys Ala Ala Lys Asp Leu Lys Asp Tyr Leu Asp
 225 230 235 240
 Lys Leu Ile Glu Glu Arg Arg Glu Thr Leu Glu Pro Ala Gly Asp Pro
 245 250 255
 Arg Arg Leu Asp Ile Gly Phe Leu Asp Ser Leu Leu Leu Glu Ala Lys
 260 265 270
 Arg Glu Gly Gly Asn Pro Lys Ser Glu Leu Ser Asp Glu Glu Leu Ala
 275 280 285
 Ala Thr Val Leu Asp Leu Leu Phe Ala Gly Thr Glu Thr Thr Ser Ser
 290 295 300
 Thr Leu Ser Trp Ala Leu Tyr Leu Leu Ala Lys His Pro Glu Val Gln
 305 310 315 320
 Ala Lys Leu Arg Glu Glu Ile Asp Glu Val Ile Gly Arg Asp Arg Ser
 325 330 335
 Pro Thr Tyr Asp Val Asp Ala Arg Ala Gln Met Pro Tyr Leu Asp Ala
 340 345 350
 Val Ile Lys Glu Thr Leu Arg Leu Tyr Pro Val Val Pro Leu Leu Leu

<400> 6

Gly Leu Pro Val Val Gly Thr Leu Val Asp Leu Ile Ala Ala Gly Gly
1 5 10 15
Ala Thr His Leu His Lys Tyr Ile Asp Ala Arg His Lys Gln Tyr Gly
20 25 30
Pro Ile Phe Arg Glu Arg Leu Gly Gly Thr Gln Asp Ala Val Phe Val
35 40 45
Ser Ser Ala Asn Leu Met Arg Gly Val Phe Gln His Glu Gly Gln Tyr
50 55 60
Pro Gln His Pro Leu Pro Asp Ala Trp Thr Leu Tyr Asn Gln Gln His
65 70 75 80
Ala Cys Gln Arg Gly Leu Phe Phe Met Glu Gly Ala Glu Trp Leu His
85 90 95
Asn Arg Arg Ile Leu Asn Arg Leu Leu Asn Gly Asn Leu Asn Trp
100 105 110
Met Asp Val His Ile Glu Ser Cys Thr Arg Arg Met Val Asp Gln Trp
115 120 125
Lys Arg Arg Thr Ala Glu Ala Ala Ala Ile Pro Leu Ala Glu Ser Gly
130 135 140
Glu Ile Arg Ser Tyr Glu Leu Pro Leu Leu Glu Gln Gln Leu Tyr Arg
145 150 155 160
Trp Ser Ile Glu Val Leu Cys Cys Ile Met Phe Gly Thr Ser Val Leu
165 170 175
Thr Cys Pro Lys Ile Gln Ser Ser Leu Asp Tyr Phe Thr Gln Ile Val
180 185 190
His Lys Val Phe Glu His Ser Ser Arg Leu Met Thr Phe Pro Pro Arg
195 200 205
Leu Ala Gln Ile Leu Arg Leu Pro Ile Trp Arg Asp Phe Glu Ala Asn
210 215 220
Val Asp Glu Val Leu Arg Glu Gly Ala Ala Ile Ile Asp His Cys Ile
225 230 235 240
Arg Val Gln Glu Asp Gln Arg Arg Pro His Asp Glu Ala Leu Tyr His
245 250 255
Arg Leu Gln Ala Ala Asp Val Pro Gly Asp Met Ile Lys Arg Ile Phe
260 265 270
Val Asp Leu Val Ile Ala Ala Gly Asp Thr Thr Ala Phe Ser Ser Gln
275 280 285
Trp Ala Leu Phe Ala Leu Ser Lys Glu Pro Arg Leu Gln Gln Arg Leu
290 295 300
Ala Lys Glu Arg Ala Thr Asn Asp Ser Arg Leu Met His Gly Leu Ile
305 310 315 320
Lys Glu Ser Leu Arg Leu Tyr
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<210> 7

<211> 87

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 7

Leu Ala Asp Ile Pro Gly Pro Gly Thr Leu Arg Phe Leu Phe Gln Leu
1 5 10 15
Phe Cys Lys Gly Tyr Leu Leu His Leu His Glu Leu Gln Val Leu Gly

			20					25					30			
Lys	Ala	Arg	Tyr	Gly	Pro	Met	Trp	Met	Ser	Ser	Phe	Gly	Thr	Gln	Arg	
		35					40					45				
Thr	Val	Asn	Leu	Ala	Ser	Pro	Pro	Leu	Val	Glu	Gln	Val	Met	Arg	Gln	
	50					55					60					
Glu	Gly	Lys	Tyr	Pro	Val	Arg	Cys	Ser	Phe	Glu	Pro	Trp	Lys	Glu	His	
65					70					75					80	
Arg	Arg	Arg	His	Gln	Arg	Ala										
				85												

<210> 8

<211> 82

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 8

Asp	Leu	Gln	Lys	Leu	Pro	Tyr	Leu	Asp	Ala	Val	Ile	Lys	Glu	Thr	Leu	
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Arg	Leu	His	Pro	Pro	Val	Pro	Thr	Val	Met	Arg	Lys	Val	Lys	Lys	Asp	
			20					25					30			
Met	Glu	Val	Ser	Gly	Thr	Val	Gly	Gly	Glu	Tyr	Thr	Ile	Pro	Lys	Gly	
		35					40					45				
Thr	Gln	Val	Met	Val	Ser	Pro	Tyr	Val	Met	Thr	His	Arg	Asp	Pro	Glu	
	50					55					60					
Tyr	Tyr	Pro	Asp	Pro	Glu	Glu	Phe	Asn	Pro	Glu	Arg	Trp	Leu	Glu	Pro	
65					70					75					80	
Ser	Glu															

<210> 9

<211> 319

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 9

Lys	Gln	Tyr	Gly	Pro	Ile	Phe	Arg	Phe	Gln	Met	Gly	Arg	Gln	Pro	Leu	
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Ile	Ile	Ile	Ala	Glu	Ala	Glu	Leu	Cys	Arg	Glu	Val	Gly	Ile	Lys	Lys	
			20					25					30			
Phe	Lys	Asp	Leu	Pro	Asn	Arg	Ser	Ile	Pro	Ser	Pro	Ile	Ser	Ala	Ser	
		35					40					45				
Pro	Leu	His	Lys	Lys	Gly	Leu	Phe	Phe	Thr	Arg	Asp	Lys	Arg	Trp	Ser	
	50					55					60					
Lys	Met	Arg	Asn	Thr	Ile	Leu	Ser	Leu	Tyr	Gln	Pro	Ser	His	Leu	Thr	
65					70					75					80	
Ser	Leu	Ile	Pro	Thr	Met	His	Ser	Phe	Ile	Thr	Ser	Ala	Thr	His	Asn	
				85					90					95		
Leu	Asp	Ser	Lys	Pro	Arg	Asp	Ile	Val	Phe	Ser	Asn	Leu	Phe	Leu	Lys	
			100					105					110			
Leu	Thr	Thr	Asp	Ile	Ile	Gly	Gln	Ala	Ala	Phe	Gly	Val	Asp	Phe	Gly	
			115				120						125			

Leu	Ser	Gly	Lys	Lys	Pro	Ile	Lys	Asp	Val	Glu	Val	Thr	Asp	Phe	Ile
130						135					140				
Asn	Gln	His	Val	Tyr	Ser	Thr	Thr	Gln	Leu	Lys	Met	Asp	Leu	Ser	Gly
145				150						155					160
Ser	Leu	Ser	Ile	Ile	Leu	Gly	Leu	Leu	Ile	Pro	Ile	Leu	Gln	Glu	Pro
			165						170					175	
Phe	Arg	Gln	Val	Leu	Lys	Arg	Ile	Pro	Gly	Thr	Met	Asp	Trp	Arg	Val
			180					185					190		
Glu	Lys	Thr	Asn	Ala	Arg	Leu	Ser	Gly	Gln	Leu	Asn	Glu	Ile	Val	Ser
		195					200					205			
Lys	Arg	Ala	Lys	Glu	Ala	Glu	Thr	Asp	Ser	Lys	Asp	Phe	Leu	Ser	Leu
	210					215					220				
Ile	Leu	Lys	Ala	Arg	Glu	Ser	Asp	Pro	Phe	Ala	Lys	Asn	Ile	Phe	Thr
225				230						235					240
Ser	Asp	Tyr	Ile	Ser	Ala	Val	Thr	Tyr	Glu	His	Leu	Leu	Ala	Gly	Ser
			245						250					255	
Ala	Thr	Thr	Ala	Phe	Thr	Leu	Ser	Ser	Val	Leu	Tyr	Leu	Val	Ser	Gly
			260					265					270		
His	Leu	Asp	Val	Glu	Lys	Arg	Leu	Leu	Gln	Glu	Ile	Asp	Gly	Phe	Gly
		275					280					285			
Asn	Arg	Asp	Leu	Ile	Pro	Thr	Ala	His	Asp	Leu	Gln	His	Lys	Phe	Pro
	290					295					300				
Tyr	Leu	Asp	Gln	Val	Ile	Lys	Glu	Ala	Met	Arg	Phe	Tyr	Met	Val	
305					310					315					

<210> 10

<211> 138

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 10

Ala	Ile	Pro	Gly	Pro	Arg	Gly	Pro	Phe	Gly	Met	Gly	Asn	Leu	Tyr	Asn
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Tyr	Leu	Pro	Gly	Ile	Gly	Ser	Tyr	Ser	Trp	Leu	Arg	Leu	His	Gln	Ala
			20					25					30		
Gly	Gln	Asp	Lys	Tyr	Glu	Lys	Tyr	Gly	Ala	Ile	Val	Arg	Glu	Thr	Ile
		35					40					45			
Val	Pro	Gly	Gln	Asp	Ile	Val	Trp	Leu	Tyr	Asp	Pro	Lys	Asp	Ile	Ala
	50					55					60				
Leu	Leu	Leu	Asn	Glu	Arg	Asp	Cys	Pro	Gln	Arg	Arg	Ser	His	Leu	Ala
65					70					75				80	
Leu	Ala	Gln	Tyr	Arg	Lys	Ser	Arg	Pro	Asp	Val	Tyr	Lys	Thr	Thr	Gly
			85						90					95	
Leu	Leu	Pro	Thr	Asn	Gly	Pro	Glu	Trp	Trp	Arg	Ile	Arg	Ala	Gln	Val
		100						105					110		
Gln	Lys	Glu	Leu	Ser	Ala	Pro	Lys	Ser	Val	Arg	Asn	Phe	Val	Arg	Gln
	115						120					125			
Val	Asp	Gly	Val	Thr	Lys	Glu	Phe	Ile	Arg						
130						135									

<210> 11

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 11

Thr	Glu	Leu	Tyr	Asp	Leu	Tyr	Ile	Arg	Glu	Ser	Met	Glu	Lys	Tyr	Gly
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Ala	Val	Lys	Phe	Phe	Phe	Gly	Ser	Arg	Trp	Asn	Ile	Leu	Val	Ser	Arg
			20					25					30		
Ser	Glu	Tyr	Leu	Ala	Gln	Ile	Phe	Lys	Asp	Glu	Asp	Thr	Phe	Ala	Lys
		35					40					45			
Ser	Gly	Asn	Gln	Lys	Lys	Ile	Pro	Tyr	Ser	Ala	Leu	Ala	Ala	Tyr	Thr
	50					55					60				
Gly	Asp	Asn	Val	Ile	Ser	Ala	Tyr	Gly	Ala	Val	Trp	Arg	Asn	Tyr	Arg
65				70						75				80	
Asn	Ala	Val	Thr	Asn	Gly	Leu	Gln	His	Phe	Asp	Asp	Ala	Pro	Ile	Phe
				85					90					95	
Lys	Asn	Ala	Lys	Ile	Leu	Cys	Thr	Leu	Ile	Lys	Asn	Arg	Leu	Leu	Glu
			100					105					110		
Gly	Gln	Thr	Ser	Ile	Pro	Met	Gly	Pro	Leu	Ser	Gln	Arg	Met	Ala	Leu
		115					120					125			
Asp	Asn	Ile	Ser	Gln	Val	Ala	Leu	Gly	Phe	Asp	Phe	Gly	Ala	Leu	Thr
	130					135					140				
His	Glu	Lys	Asn	Ala	Phe	His	Glu	His	Leu	Ile	Arg	Ile	Lys	Lys	Gln
145				150					155					160	
Ile	Phe	His	Pro	Phe	Phe	Leu	Thr	Phe	Pro	Phe	Leu	Asp	Val	Leu	Pro
				165					170					175	
Ile	Pro	Ser	Arg	Lys	Lys	Ala	Phe	Lys	Asp	Val	Val	Ser	Phe	Arg	Glu
		180						185					190		
Leu	Leu	Val	Lys	Arg	Val	Gln	Asp	Glu	Leu	Val	Asn	Asn	Tyr	Lys	Phe
		195					200					205			
Glu	Gln	Thr	Thr	Phe	Ala	Ala	Ser	Asp	Leu	Ile	Arg	Ala	His	Asn	Asn
	210					215					220				
Glu	Ile	Ile	Asp	Tyr	Lys	Gln	Leu	Thr	Asp	Asn	Ile	Val	Ile	Ile	Leu
225				230						235				240	
Val	Ala	Gly	His	Glu	Asn	Pro	Gln	Leu	Leu	Phe	Asn	Ser	Ser	Leu	Tyr
			245						250					255	
Leu	Leu	Ala	Lys	Tyr	Ser	Asn	Glu	Trp	Gln	Glu	Lys	Leu	Arg	Lys	Glu
		260					265						270		
Val	Asn	Gly	Ile	Thr	Asp	Pro	Lys	Gly	Leu	Ala	Asp	Leu	Pro	Leu	Leu
	275					280						285			
Asn	Ala	Phe	Leu	Phe	Glu	Val	Val	Arg	Met	Tyr	Pro	Pro	Leu		
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<210> 12

<211> 138

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<213> Artificial Sequence

<220>

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<400> 12

Leu	Arg	Gln	Val	Gln	Asp	Glu	Thr	Ile	Arg	Leu	Ser	Thr	Leu	Ala	Pro
1				5					10					15	
Trp	Ala	Ala	Arg	Tyr	Ser	Asp	Lys	Lys	Val	Thr	Val	Cys	Gly	Tyr	Thr
			20					25					30		

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Ile Pro Ala Lys Thr Pro Met Ile His Ala Leu Gly Val Gly Leu Lys
    35              40              45
Asn Lys Thr Val Trp Glu Asn Thr Asp Ser Trp Asp Pro Asp Arg Phe
    50              55              60
Ser Pro Asn Gly Arg Arg Gly Asn Asp Phe Cys Pro Phe Gly Val His
    65              70              75              80
Ser Arg Arg Lys Cys Pro Gly Tyr Leu Phe Ser Tyr Phe Glu Val Gly
    85              90              95
Val Phe Ala Ser Ile Leu Leu Ser Arg Phe Glu Ile Val Pro Val Glu
    100             105             110
Gly Gln Thr Val Ile Gln Val His Gly Leu Val Thr Glu Pro Lys Asp
    115             120             125
Asp Ile Lys Ile Tyr Ile Arg Ser Arg Lys
    130             135

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<210> 13
 <211> 67
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<220>
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<400> 13
Ile Ala Gly Met Asp Thr Ala Ala Asn Ser Leu Ala Phe Val Leu Tyr
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Arg Met His Leu His Ser Glu Phe Leu Pro Ala Leu Arg Ala Glu Ala
    20              25              30
Asp Ala Leu Phe Arg Asp Gly Pro Pro Thr Ala Glu Ala Leu Gly Arg
    35              40              45
Ser Pro Leu Leu His Arg Phe Val Met Glu Thr Leu Arg Val His Pro
    50              55              60
Ile Ala Pro
65

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<210> 14
 <211> 95
 <212> PRT
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<400> 14
Val Pro Ala Pro Pro Phe Leu Gly His Ala Ala Glu Met Gly Thr Ile
  1              5              10              15
Lys Leu Arg Pro Phe Leu Thr Arg Cys Tyr Gln Ala Tyr Gly Pro Val
    20              25              30
Phe Gln Leu Thr Val Pro Gly Gln Lys Ile Thr Val Leu Ala Gly Pro
    35              40              45
Glu Ala Asn Leu Phe Ala Met Lys Glu Gly His Arg Val Leu Arg Ser
    50              55              60
Leu Glu Ala Trp Arg Asp Asn Asp His Glu Met Gly Ser Asp Arg Ser
    65              70              75              80
Met Ile Ser Leu Asp Gly Ala Glu His Arg Ala Tyr Arg Arg Val
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<210> 15
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<220>
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<400> 15
 Thr Val Ala Ile Ser Pro Tyr Gly Glu Gln Trp Lys Lys Met Arg Lys
 1 5 10 15
 Val Ile Thr Thr Glu Ile Met Ser Pro Lys Arg Leu Asn Trp Leu Leu
 20 25 30
 Gly Lys Arg Thr Glu Glu Ala Asp Asn Leu Val Ala Tyr Val His Asn
 35 40 45
 Met Cys Gln Lys Ser Glu Thr Asn Asn Lys His Gly Ala Val Ile Asp
 50 55 60
 Val Arg Asp Val Val Arg His Tyr Cys His Asn Val Val Met Arg Met
 65 70 75 80
 Met Phe Gly Arg Arg His Phe Gly Lys Gly Thr Glx Phe Ser Asp Asp
 85 90 95
 Gly Gly Pro Gly Pro Glu Glu Lys Glu His Met Asp Ala Ile Phe Thr
 100 105 110
 Ala Leu Asp Cys Leu Tyr Ala Phe Cys Val Ser Asp Tyr Ile Pro Arg
 115 120 125
 Trp Leu Arg
 130

<210> 16
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 16
 Arg Trp Leu Arg Gly Trp Asp Leu Asp
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